

FIGURE !

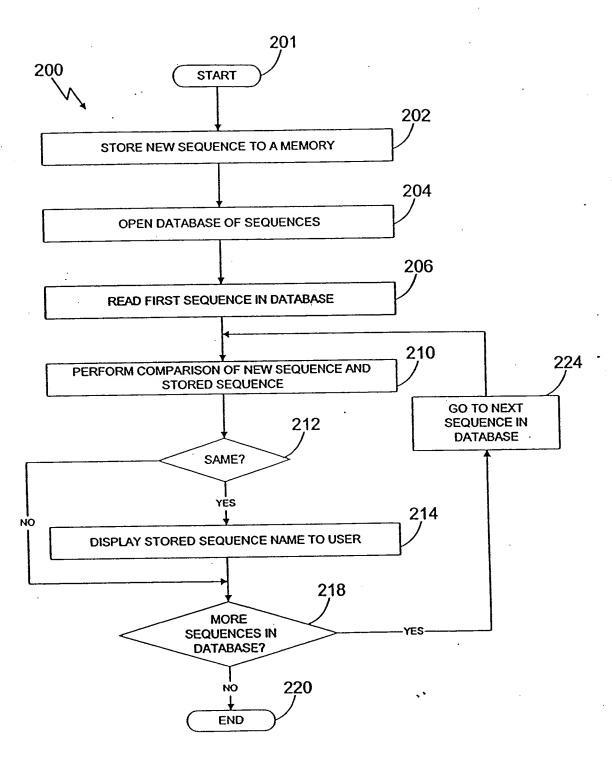
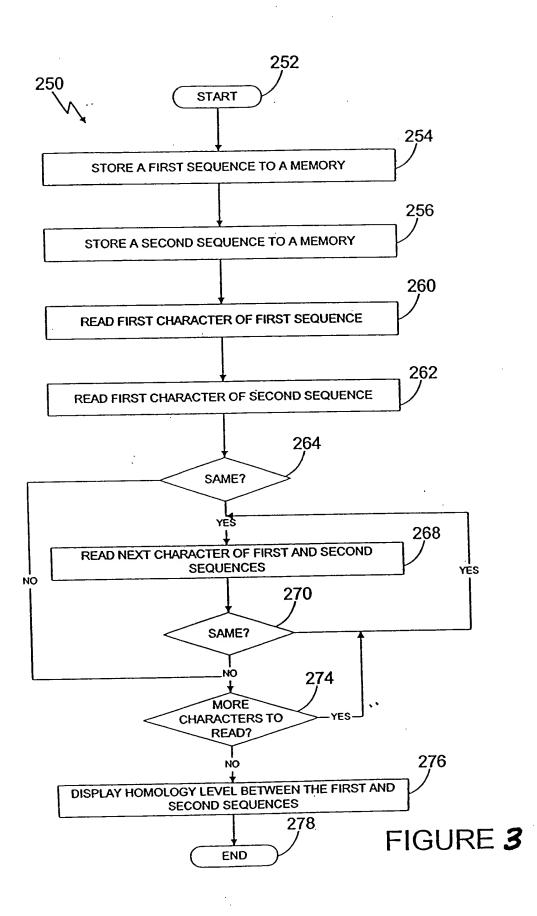
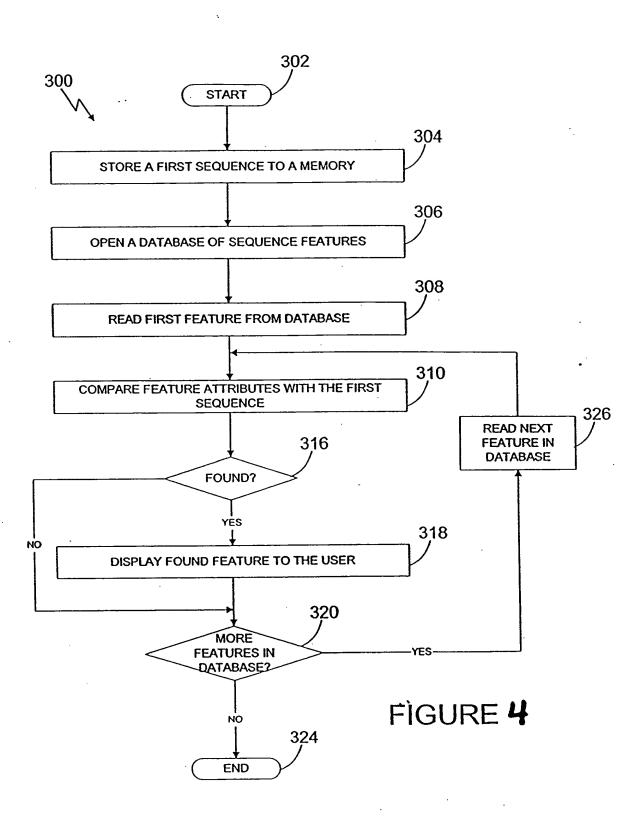


FIGURE 2





Catalase - 64CA2 Alcaligenes (Deleya) aquamarinus

(SEQ ID NO: 5) (SEQ ID NO: 6)

180 60 240 80 GGT TTG 360 Gly Leu 120 GGG GGC 420 Gly Gly 140 GTC CAC 300 Val His 100 GAA GAT ATG AAT AAC GCA TCC GCT GAC GAT CTA CAC AGT AGC TTG CAG CAA AGA TGC AGA GCA . Met Asn Asn Ala Ser Ala Asp Asp Leu His Ser Ser Leu Gln Gln Arg Cys Arg Ala . AAA Lys(CCG (Pro) GAT (Trb GAT (GGC GLV CCG ATG Pro Met A CAC TAC (His Tyr (TGG 7 GCT ATG AGC Ala Met Ser CTG AAG AAA Leu Lys Lys GAT Asp TGG GGG (Trb Gly F GAC (ASp) GGT ACT TCC AAC AAA GIY Thr Ser Asn Lys. TCA(GCG (Ala] GCA ATA AGG GAG AGA Ala Ile Arg Glu Arg GAT CGC AAA' Asp Arg Lys GAC'ASP' GAT TTC GAC Asp Phe Asp GCT CCC (Pro / TGG TGG CTC CAA Gln. GGT AAC ACC TCG ACC GIY Asn Thr Ser Thr CAG Gln CCC TTG GTA TCG CCA AGG CAT AGA Pro Leu Val Ser Pro Arg His Arg GAA GTA CGC AAG Glu Val Arg Lys GAG CTGGAT ATT TTGCAT Leu Asp Ile Leu His CAA (GIn (AGC (Ser (GGT (GAA (GAT ASP CGT (CCT GTC ATG CAC Pro Val Met His TTG ATG ACC Leu Met Thr GGG TTG AAC GIy Leu Asn TTC AAC TAC Phe Asn Tyr GTT GCG. 181 61 301 241

250 220 20 20 20 GCT TAC (Ala Tyr) GAC (ASp.) GGT CCT GAT ATC TAC TGG ASP I LE TYY TYP TTA 990 617 TCC ATG (Ser Met (GAA AAA G Glu Lys A TATGAG CCC (Pro (GAA (GCT ATT TGG ACC GTG (Thr Val F 647 617 617 CGC GTC GAT Arg Val Asp GCT CTG (Lear) 66C(CTGATGATT Leu Met Ile TTC (Phe (TTC TCT Phe Ser GAC (ASp) GCA 900 017 017 541 181 601 201

1480 160 160

CTG /

AGC (Ser]

GTC

AAC (ASn

GAC ASP

CCG (Pro 7

Tro]

Sec

CTC AAC Leu Asn

CCG

GCA Ala

TTT (Phe /

CGC A

CAG

AGC

GGA Z

GGT ACC (

GGT

477

GGC CGT (G1y Arg (

GAT (ASP (

ACC TAC CGT ATT GCT. Thr Tyr Arg Ile Ala.

990 614

GCT

TCC (Ser/

CAC' His

TGG Trp]

GCT

Arg Met A

ATC (In Inc.)

ATG. Met

361

54(18(

AGC TGG

AAA L Lys

AAC A

GGC 7

TAC (Tyr (

AAG AAG AAG Lys Lys Lys

AIC

CCG 7

Tro Tro

CTG CTG Leu Leu

CGT

CGC (

GCG Ala

AAA (Lysi

GAT. Asp

61

FIGURE 6

Microscilla furvescens Catalase - 53CA

(SEQIDNO:7) (SEQIDNO:8)

AAA Lys (ACT GGC (Thr Gly (ACA AAC Thr Asn AAC A ACG TAT TCT. TCT TCA AAA CAC Lys His GAA AAT CAC Glu Asn His ATG (Met (

120 Trp GAT'ASP' AGG Arg AAC Asn AAA Lys GGCACC 990 614 614 GGT GCA AGT CAA AAG Lys CTT / GGT TCG (GLy Ser I GGA ACC TTT, Phe CCT Pro

180 60 AAC CCA GACASP TCG. Ser. CIA Ser TCA CAT CAA CGC TTA (Leu i AIC 990 614 CTC AAC (Leu Asn] ATG Met AAC. Asn CCC / Trp 127

240 80 AAG; Lys AAA Lys GTT Val GCG GCA CTG GAT CTA (Leu/ AAG AAG Z Lys J TTT GAG'GIU GAA GCC TAT GAC TTT (Phe.) GAT CCG Pro GAC , 6 19 8

300 CAT TAT His Tyr GGT TAC GAT ASP GCA Ala CCA (Pro) TGG TGG GAC CAG TCA (GAT ATG ACA (Met Thr CTA Z GCG (GCA (CTG (Lea i GAC 女こ

360 120 000 0100 GAT (ASP) GGT AIC CGT / TAC ACC 900 000 010 GCC AGC CAC Trp GCG GGC ATG CARG Arg Met A ATA (Ile i TTT TTC CCC 660 610 301

420 140 AAT GAC. Asp. CCA TGG (Trb) AGC Ser AAT CTC. CCT GCG TTC CGC CAG (GIn TCA (Ser (66C 61Y TCC 66C 610 GGT 930 617 617 GGT (CGT 361

180 160 CGA AAA GGT TAC AAA Lys Glab AAA Lys (ATC 110 CCC Trp CTT CTT (TIG CGC GCA AAA (Lysi GAT CTG (AAT GCC 1421

540 180 TTT Phe ATG Met ACT I GAA CTG (GCT GTA Val AAC GGA ACA CTC / ATA (Ile CTA ATG / Leu Met] GAT GCG (Alai Tro TCC. ATC Ile 181 161

200 GTA TAC GAT GAA GAA CCT GAG Glu Trp GTA GAT (GCA AGA (GGT GCA Ala TTT Phe. GGT TTT ACT AAA Lys 541 181

220 220 GAA CIC GAG CGA (Arg (GAC (ASp. 1 GGT GAA TAT CGC AAG (Lys) GAC GGA (CTG Trp GAA G ACC GAA GGA TGG (Trb)

